

WHAT IS CLAIMED IS:

1                   1.       A method of typing a growth arising in association with a congenital  
2 melanocytic nevus, the method comprising providing a skin tumor sample from a patient and  
3 detecting a change in chromosome number in a nucleic acid sample from the skin tumor  
4 sample, wherein the change in chromosome number is selected from the group consisting of a  
5 gain of chromosome 10, a gain of chromosome 11, a loss of chromosome 7, or a combination  
6 thereof; thereby typing the skin tumor sample as a benign growth.

1                   2.       The method of claim 1, wherein the change in chromosome number is  
2 a gain of chromosome 10.

1                   3.       The method of claim 1, wherein the change in chromosome number is  
2 a gain of chromosome 11.

1                   4.       The method of claim 1, wherein the change in chromosome number is  
2 a loss of chromosome 7.

1                   5.       The method of claim 1, further comprising detecting a gain or loss of  
2 another chromosome.

1                   6.       The method of claim 1, wherein the detecting step comprises:  
2                   contacting a nucleic acid sample from the patient with a probe which  
3 selectively hybridizes to a target polynucleotide sequence on a chromosome selected from the  
4 group consisting of chromosome 10, chromosome 11, and chromosome 7; wherein the probe  
5 is contacted with the sample under conditions in which the probe binds selectively with the  
6 target polynucleotide sequence to form a stable hybridization complex;  
7                   detecting the formation of the hybridization complex; and  
8                   detecting a change in chromosome number, the change selected from the  
9 group consisting of a gain of chromosome 10, a gain of chromosome 11 and a loss of  
10 chromosome 7.

1                   7.       The method of claim 6, wherein the detecting step further comprises  
2 amplifying the target nucleotide sequence.

1                   8.       The method of claim 7, wherein the target nucleotide sequence is  
2 amplified using a polymerase chain reaction.



- 1 9. The method of claim 6, wherein the eprobe is a centromeric probe.
- 1 10. The method of claim 1, wherein the nucleic acid sample is an  
2 interphase nucleus.
- 1 11. The method of claim 1, wherein the nucleic acid sample is a metaphase  
2 cell.
- 1 12. The method of claim 6, wherein the probe is labeled with a fluorescent  
2 label.
- 1 13. The method of claim 6, wherein the probe is labeled with digoxigenin  
2 or biotin.
- 1 14. The method of claim 6, further comprising the step of blocking the  
2 hybridization capacity of repetitive sequences in the nucleic acid sample.
- 1 15. The method of claim 14, wherein unlabeled blocking nucleic acids  
2 comprising repetitive sequences are contacted with the sample.
- 1 16. The method of claim 15, wherein the unlabeled blocking nucleic acids  
2 are Cot-1 DNA.
- 1 17. The method of claim 6, wherein the probe is bound to a solid substrate.
- 1 18. The method of claim 17, wherein the probe is a member of an array.